



REPLACEMENT SHEET

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FIG. 1A

Range : 1 - 1053 Mode : Normal

Codon Table : Universal

9	18	27	36	45	54
5' ATG GGC GAC CCG GAA AGG CCG GAA GCG GCC GGG CTG GAT CAG GAT GAG AGA TCA					
Met Gly Asp Pro Glu Arg Pro Glu Ala Ala Gly Leu Asp Gln Asp Glu Arg Ser					
63	72	81	90	99	108
TCT TCA GAC ACC AAC GAA AGT GAA ATA AAG TCA AAT GAA GAG CCA CTC CTA AGA					
Ser Ser Asp Thr Asn Glu Ser Glu Ile Lys Ser Asn Glu Glu Pro Leu Leu Arg					
117	126	135	144	153	162
AAG AGT TCT CGC CGG TTT GTC ATC TTT CCA ATC CAG TAC CCT GAT ATT TGG AAA					
Lys Ser Ser Arg Arg Phe Val Ile Phe Pro Ile Gln Tyr Pro Asp Ile Trp Lys					
171	180	189	198	207	216
ATG TAT AAA CAG GCA CAG GCT TCC TTC TGG ACA GCA GAA GAG GTC GAC TTA TCA					
Met Tyr Lys Gln Ala Gln Ala Ser Phe Trp Thr Ala Glu Glu Val Asp Leu Ser					
225	234	243	252	261	270
AAG GAT CTC CCT CAC TGG AAC AAG CTT AAA GCA GAT GAG AAG TAC TTC ATC TCT					
Lys Asp Leu Pro His Trp Asn Lys Leu Lys Ala Asp Glu Lys Tyr Phe Ile Ser					
279	288	297	306	315	324
CAC ATC TTA GCC TTT TTT GCA GCC AGT GAT GGA ATT GTA AAT GAA AAT TTG GTG					
His Ile Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Asn Glu Asn Leu Val					
333	342	351	360	369	378
GAG CGC TTT AGT CAG GAG GTG CAG GTT CCA GAG GCT CGC TGT TTC TAT GGC TTT					
Glu Arg Phe Ser Gln Glu Val Gln Val Pro Glu Ala Arg Cys Phe Tyr Gly Phe					
387	396	405	414	423	432
CAA ATT CTC ATC GAG AAT GTT CAC TCA GAG ATG TAC AGT TTG CTG ATA GAC ACT					
Gln Ile Leu Ile Glu Asn Val His Ser Glu Met Tyr Ser Leu Leu Ile Asp Thr					

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FIG. 1B

441	450	459	468	477	486
TAC	ATC	AGA	GAT	CCC	AAG
AAA	AGG	GAA	TTT	TTA	TTT
AAT	GCA	ATT	GAA	ACC	ATG

Tyr	Ile	Arg	Asp	Pro	Lys
Lys	Arg	Glu	Phe	Leu	Phe
Asn	Ala	Ile	Glu	Thr	Met

495	504	513	522	531	540
CCC	TAT	GTT	AAG	AAA	AAA
GCA	GAT	TGG	GCC	TTG	CGA
TGG	ATA	GCA	GAT	AGA	AAA

Pro	Tyr	Val	Lys	Lys	Lys
Ala	Asp	Trp	Ala	Leu	Arg
Trp	Ile	Ala	Asp	Arg	Lys

549	558	567	576	585	594
TCT	ACT	TTT	GGG	GAA	AGA
GTG	GTG	GCC	TTT	GCT	GCT
GTA	GAA	GGA	GTT	TTC	TTC

Ser	Thr	Phe	Gly	Glu	Arg
Val	Val	Ala	Phe	Ala	Ala
Val	Glu	Gly	Val	Phe	Phe

603	612	621	630	639	648
TCA	GGA	TCT	TTT	GCT	GCT
ATA	TTC	TGG	CTA	AAG	AAG
AGA	GGT	CTT	ATG	CCA	GGA

Ser	Gly	Ser	Phe	Ala	Ala
Ile	Phe	Trp	Leu	Lys	Lys
Arg	Gly	Leu	Met	Pro	Gly

657	666	675	684	693	702
CTC	ACT	TTT	TCC	AAT	GAA
CTC	ATC	AGC	AGA	GAT	GAA
GGA	CTT	CAC	TGT	GAC	TTT

Leu	Thr	Phe	Ser	Asn	Glu
Leu	Ile	Ser	Arg	Asp	Glu
Gly	Leu	His	Cys	Asp	Phe

711	720	729	738	747	756
GCT	TGC	CTG	ATG	TTC	CAA
TAC	TTA	GTA	AAT	AAG	CCT
TCA	GAA	GAA	AGG	GTC	AGG

Ala	Cys	Leu	Met	Phe	Gln
Tyr	Leu	Val	Asn	Lys	Pro
Ser	Glu	Glu	Arg	Val	Arg

765	774	783	792	801	810
GAG	ATC	ATT	GTT	GAT	GCT
GTC	AAA	ATT	GAG	CAG	GAG
TTT	TTA	ACA	GAA	GCC	TTG

Glu	Ile	Ile	Val	Asp	Ala
Val	Lys	Ile	Glu	Gln	Glu
Phe	Leu	Thr	Glu	Ala	Leu

819	828	837	846	855	864
CCA	GTT	GGC	CTC	ATT	GGA
ATG	AAT	TGC	ATT	TTG	ATG
AAA	CAG	TAC	ATT	GAG	TTT

Pro	Val	Gly	Leu	Ile	Gly
Met	Asn	Cys	Ile	Leu	Met
Lys	Gln	Tyr	Ile	Glu	Phe

873	882	891	900	909	918
GTA	GCT	GAC	AGA	TTA	CTT
GTG	GAA	CTT	GGA	TTG	TCA
AAG	GTT	TTT	CAG	GCA	GAA

Val	Ala	Asp	Arg	Leu	Leu
Val	Glu	Leu	Gly	Phe	Ser
Lys	Val	Phe	Gln	Ala	Glu

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FIG. 1C

927	936	945	954	963	972
AAT CCT TTT GAT TTT ATG GAA AAC ATT TCT TTA GAA GGA AAA ACA AAT TTC TTT					

Asn Pro Phe Asp Phe Met Glu Asn Ile Ser Leu Glu Gly Lys Thr Asn Phe Phe					

981	990	999	1008	1017	1026
GAG AAA CGA GTT TCA GAG TAT CAG CGT TTT GCA GTT ATG GCA GAA ACC ACA GAT					

Glu Lys Arg Val Ser Glu Tyr Gln Arg Phe Ala Val Met Ala Glu Thr Thr Asp					

1035	1044	1053
AAC GTC TTC ACC TTG GAT GCA GAT TTT 3'		

Asn Val Phe Thr Leu Asp Ala Asp Phe		

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Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1 (1>351)	Seq2 (1>389)	Similarity
Tp53r2h. pro	R2. pro	Index
(15>351)	(53>389)	80. 4
(1>351)	(39>389)	77. 5

	10	20	30	40	50	60	70	80
TP53R2H	MGDPERPEAAGLDQDERSSSDTNESEIKSNEEPLLKSSRRFVIFPIQYPD	IWKMYKQAQASFWTAAEEVDLSKDLP	HWNK					
R2	GTRVLASKTARRIFQEPT	PKTKAAAPGVEDEPLLR	ENPRRFVIFPIEYHDI	WQMYKKA	EASFWTAAEEVDLSKD	I	QHWES	
	40	50	60	70	80	90	100	110
	90	100	110	120	130	140	150	160
TP53R2H	LKADEKYFISHILAFFAASDGI	VNENLVERFSQEVQVPEARCFYGFQIL	ENHSEMYSL	IDTYIRDPKKREF	LNAIE			
R2	LKPEERYFISHVLAFFAASDGI	VNENLVERFSQEVQITEARCFYGFQI	AMENIHSEMYSL	IDTYIKDPKEREFL	NAIE			
	120	130	140	150	160	170	180	190
	170	180	190	200	210	220	230	240
TP53R2H	TMPYVKKKADWALRWI	ADRKSTFGERVVAFAAVEGVFFSGSFAAIFWLKKRGLMPGLTFSNEL	ISRDEGLHCDFA	CLMFQ				
R2	TMPCVKKKADWALRWI	GDKEATYGERVVAFAAVEGIFFSGSFASIFWLKKRGLMPGLTFSNEL	ISRDEGLHCDFA	CLMFK				
	200	210	220	230	240	250	260	270
	250	260	270	280	290	300	310	320
TP53R2H	YLVNKPSEERVREIIVDAVKIEQ	EFLTEALPVGLIGMNCILMKQYIEFVADRLLVELGFSKVQ	AENPFDFMENISLEGK					
R2	HLVHKPSEERVREIINAVRIEQ	EFLTEALPVKILGMNCTLMKQYIEFVADRMLLELGF	SKVFRVENPFDFMENISLEGK					
	280	290	300	310	320	330	340	350
	330	340	350					
TP53R2H	TNFFEKR	VSEYQRF	AVMAETTDNVFTLDADF					
R2	TNFFEKR	VGEYQRM	GVMSSPTENSFTLDADF					
	360	370	380					

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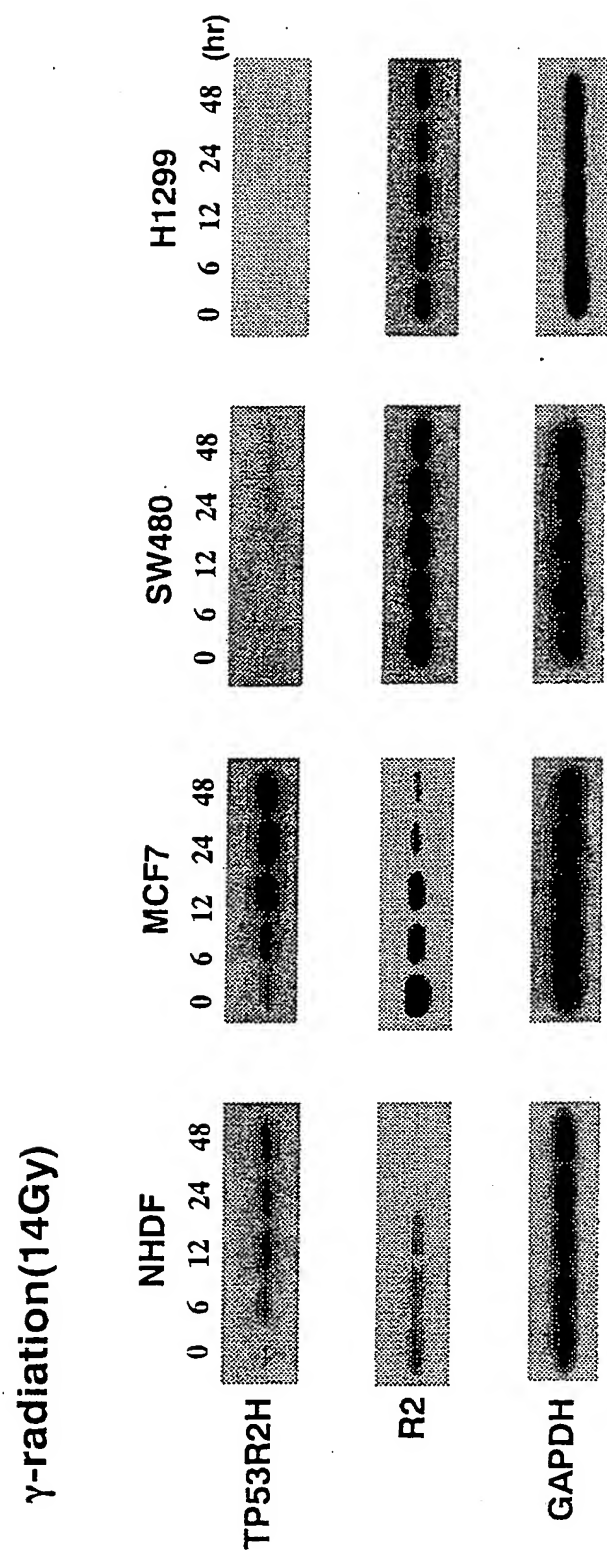


FIG. 3

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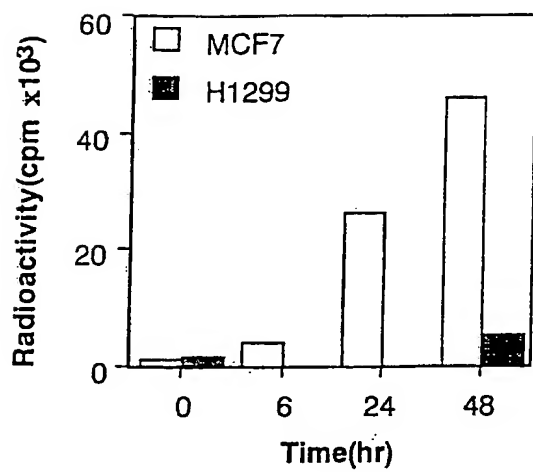


FIG. 4

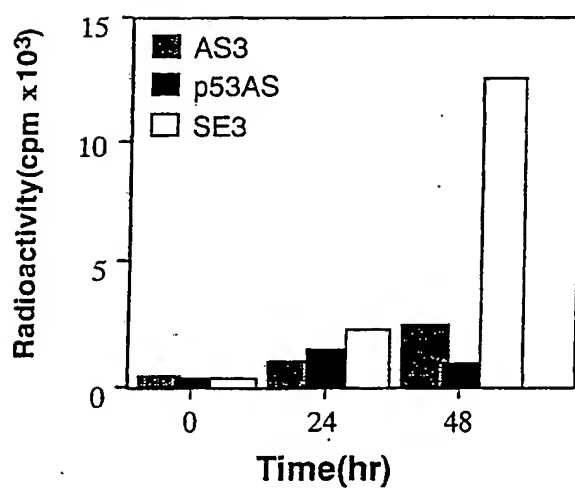


FIG. 5

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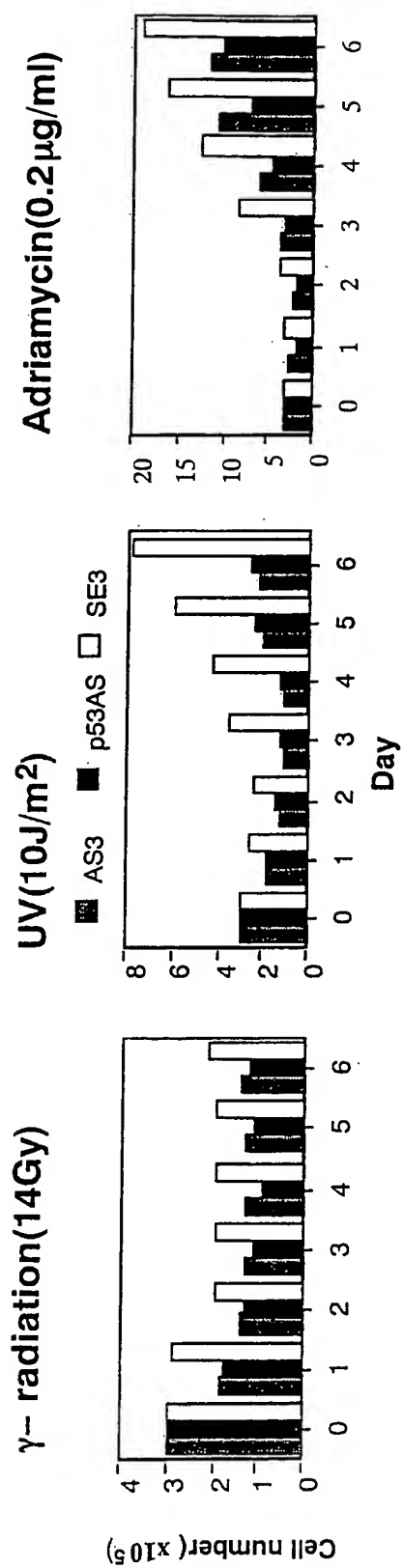


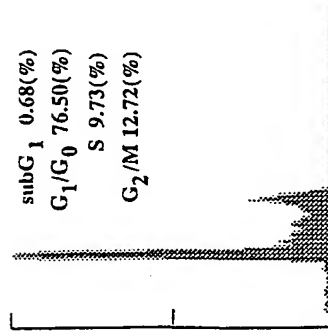
FIG. 6A

FIG. 6B

FIG. 6C

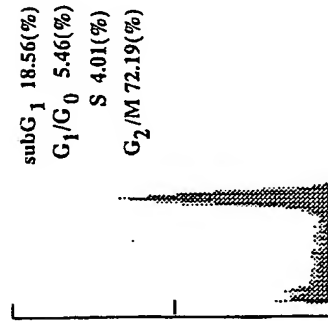
TP53R2H

pcDNA3.1(+)



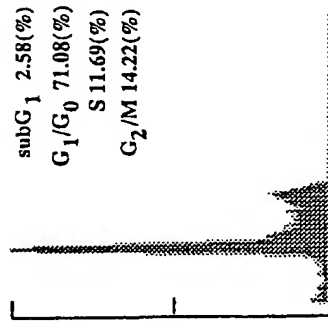
Adriamycin(0hr)

FIG. 7A



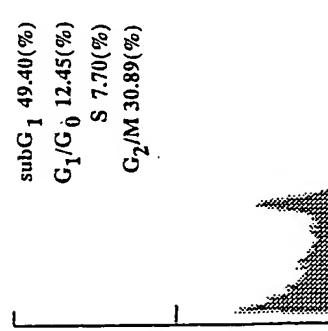
Adriamycin(48hr)

FIG. 7B



Adriamycin(0hr)

FIG. 7C



Adriamycin(48hr)

FIG. 7D